

Problem Set 3 - Proteins

**Introduction to Bioengineering**

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## Problem 1

Use the browser protein structure viewer available on RCSB.ORG or download a software to view PDB structure files:

- <http://spdbv.vital-it.ch/>
- <http://www.bernstein-plus-sons.com/software/rasmol/>
- <http://www.pymol.org/>
- <http://www.ks.uiuc.edu/Research/vmd/>

Then download the following structures from the PDB ([www.rcsb.org](http://www.rcsb.org)):

- Zif268-DNA (1AAY or 1ZAA)
- MAX - DNA (1AN2)
- TAL (3UGM, 3V6T)

Problem 1.1: Show a picture of the three transcription factors.

Problem 1.2: Measure the width of the major and minor groove of DNA. Provide an image indicating where you measured with a line. Provide a short but detailed description of how you decided to measure the width and explain and justify why you chose to measure the width that way.

Problem 1.3: Choose your favorite of the 3 structures and display a detailed view of the DNA - transcription factor binding interface and clearly indicate one non-specific and one specific interaction between the TF and DNA. Specific interactions are contacts between the protein and the nucleobases of DNA, whereas non-specific interactions are contacts between the protein and the phosphate backbone of DNA. (Hint: using the slab view feature will help to display only the parts you are interested in)

## Problem 2

Problem 2.1: Why is the  $\alpha$ -helix the dominant secondary structure used by transcription factors?

Problem 2.2: Do you expect transcription factors to bind equally well to A-DNA? Explain why or why not.